



Age disparities in intestinal stem cell quantities: a possible explanation for preterm infant susceptibility to necrotizing enterocolitis

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Abstract

Purpose Preterm infants are more susceptible to necrotizing enterocolitis (NEC) than term Queryinfants. This may be due to a relative paucity of *Lgr5*⁺ or *Bmi1*⁺-expressing intestinal stem cells (ISCs) which are responsible for promoting intestinal recovery after injury. We hypothesized that the cellular markers of *Lgr5*⁺ and *Bmi1*⁺, which represent the two distinct ISC populations, would be lower in younger mice compared to older mice. In addition, we hypothesized that experimental NEC would result in a greater loss of *Lgr5*⁺ expression compared to *Bmi1*⁺ expression.

Methods Transgenic mice with EGFP-labeled *Lgr5* underwent euthanasia at 10 different time points from E15 to P56 ($n = 8–11$ /group). *Lgr5*⁺-expressing ISCs were quantified by GFP ELISA and *Bmi1*⁺ was assessed by qPCR. In addition, *Lgr5*^{EGFP} mice underwent experimental NEC via formula feeding and hypoxic and hypothermic stress. Additional portions of the intestine underwent immunostaining with anti-GFP or anti-*Bmi1*⁺ antibodies to confirm ELISA and PCR results. For statistical analysis, $p < 0.05$ was significant.

Results *Lgr5*⁺ and *Bmi1*⁺ expression was lowest in embryonal and early postnatal mice and increased with age in all segments of the intestine. Experimental NEC was associated with loss of *Lgr5*⁺-expressing ISCs but no significant change in *Bmi1*⁺ expression.

Conclusion *Lgr5*⁺ and *Bmi1*⁺ expression increase with age. *Lgr5*⁺-expressing ISCs are lower following experimental necrotizing enterocolitis while *Bmi1*⁺ expression remains relatively unchanged. Developing a targeted medical therapy to protect the low population of ISCs in preterm infants may promote tissue recovery and regeneration after injury from NEC.

Keywords Necrotizing enterocolitis · *Lgr5* · *Bmi1* · Intestinal stem cells · Animal study

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Introduction

Necrotizing enterocolitis (NEC) is a devastating disease that affects the gastrointestinal tract of preterm infants [1]. Despite decades of research, there have been only limited advancements in understanding the complex pathophysiology associated with NEC, and even more limited advancements in the development of targeted therapies [2]. NEC often evolves rapidly and presents as abdominal distention, feeding intolerance, and sepsis [3]. Mortality is estimated at 20% in all infants with NEC, 40% for infants who require surgery, and 50% for extremely low birthweight infants who require surgery [4].

To improve outcomes in NEC and develop a targeted medical therapy, it is important to better define the pathophysiology. It is also critical to better understand why

preterm infants are more susceptible to NEC than their term counterparts. Premature infants are at high risk for the development of NEC in part due to perturbations of intestinal peristalsis [5, 6], decreased intestinal mucous production [7], leaky epithelium that allows bacteria to translocate [8], and immaturity of enzymes for digesting nutrients [9]. However, a diminished capacity for intestinal repair following injury is also highly likely, and this may be due to a relative paucity of intestinal stem cells (ISCs) [10, 11].

Intestinal stem cells play a critical role during injury, where they repair damaged tissue and repopulate the intestine with functional cells to facilitate recovery [12, 13]. This process is known as intestinal restitution. NEC often causes severe irreversible injury to the intestine of preterm infants, and this may be due to younger infants having a smaller reservoir of ISCs to replace injured epithelial cells in the gut.

There are two distinct intestinal stem cell populations that reside in the intestinal crypts. *Bmi1*⁺ (B lymphoma Mo-MLV insertion region 1 homolog) expressing cells reside at the +4 position in the crypts of the intestine, are relatively quiescent and are capable of differentiating into all cell types of the intestine [14]. In contrast to *Bmi1*⁺ cells, the *Lgr5* (leucine-rich repeat-containing G-protein coupled receptor 5) surface protein expressing ISC resides deep in the crypts of the intestinal villi and is mitotically quite active [15]. There are an estimated 4–6 *Lgr5*⁺ ISCs per crypt [16]. These intestinal stem cells divide frequently to rapidly renew the intestinal epithelium and are also progenitors to all cell types of the intestinal villi, including enterocytes, goblet cells, enteroendocrine cells, and Paneth cells [17].

It has been suggested that *Bmi1*⁺ and *Lgr5*⁺ mark an overlapping or redundant stem cell system. Transgenic mice with fluorescent-labeled *Lgr5*⁺ or *Bmi1*⁺ cells were studied in quiescent homeostatic states. *Lgr5*⁺ cells cycled more rapidly and were more efficient at generating progeny compared to *Bmi1*⁺. *Lgr5*⁺ cells also responded more robustly to *Wnt* agonists and antagonists, thereby shedding light on stimuli for rapid cell division. However, when the bowel was injured with radiation, the *Lgr5*⁺ population was eradicated quickly while the *Bmi1*⁺ population survived and expanded. *Bmi1*⁺ cells gave rise to additional *Lgr5*⁺ cells. These data suggest that the *Lgr5*⁺ population is rapidly cycling and may be more involved in homeostasis, while *Bmi1*⁺ cells are more injury resistant and help to repopulate the gut after severe injury [18].

The objective of this study was to quantify the number of *Lgr5*⁺ and *Bmi1*⁺-expressing ISCs and assess how age affects the relative abundance of these cell populations. We hypothesized that increasing age would directly correlate with the abundance of ISC markers in the duodenum, terminal ileum, and colon. In addition, we hypothesized that experimental NEC would be associated with a greater loss of *Lgr5*⁺ expression in the terminal ileum compared to *Bmi1*⁺.

Methods

Tissue procurement and genotyping

All research followed ethical guidelines under an IACUC-approved protocol at the Indiana University School of Medicine. To identify the proportion of *Lgr5*⁺-expressing ISCs, we used a mutant mouse with an enhanced green fluorescent protein (EGFP) knocked into the *Lgr5* gene locus (Genentech, San Francisco, CA). Detection of EGFP in heterozygous *Lgr5*^{EGFP} mice served as a marker of *Lgr5*⁺-expressing ISCs, as described by Tian et al. [19]. Tissue was obtained from tail cuts for genotyping. DNA was extracted with 50 mM sodium hydroxide at 95 °C for 1 h. DNA was amplified with Taq polymerase (Cat # M712B, Thermo Fisher Scientific, Waltham, MA, USA) and primers as shown in Appendix 1. Only heterozygous *Lgr5*^{EGFP} mice were used for analysis as a homozygous *Lgr5*^{EGFP} mutation is lethal (Fig. 1).

Heterozygous *Lgr5*^{EGFP} male mice were bred with female C57BL/6 J mice (Jackson Labs, Bar Harbor, ME). Timed breeding was utilized to measure the precise age of the progeny. Mice were euthanized at 2 embryonal (E) ages and 8 postnatal (P) ages: E15, E18, P1, P3, P5, P7, P14, P21, P28, and P56. For embryo tissue procurement, pregnant dams underwent carbon dioxide (CO₂) euthanasia. A midline laparotomy was performed, and embryos were removed

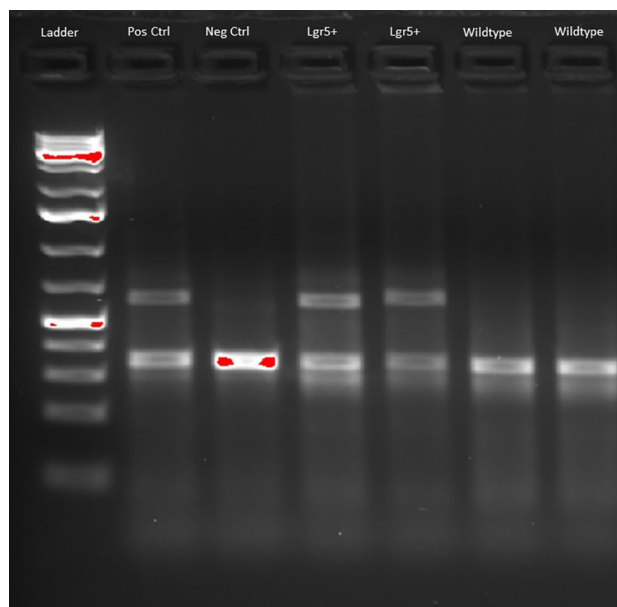


Fig. 1 PCR and immunohistochemistry of *Lgr5*. A representative PCR gel: lane 1 DNA ladder 1 kB (Cat # SM1333 Thermo Fisher Scientific, Waltham, MA, USA), lane 2 positive control, lane 3 negative control, lanes 4–5 heterozygous *Lgr5*^{EGFP}, lanes 6–7 homozygous wild type

from the uterine horns. Intestine was isolated and identified using a dissecting microscope. For E15 embryos, the gut was explanted and separated into 2 segments: ileum and colon. For all other age groups, the gut was mature enough to separate into 3 segments: duodenum, terminal ileum, and ascending colon. Pups remained with dams and breastfed until 21 days at which time they were weaned. Pups from age P1 to P7 were euthanized via cervical decapitation, and mice from P14 to P56 underwent CO₂ euthanasia.

Lgr5⁺ stem cell quantification by ELISA

Segments of the intestine were harvested immediately after euthanasia and were snap frozen in liquid nitrogen and stored at -80°C . Tissue was homogenized in a 4°C cold room. The intestine was placed into 1.5 mL Eppendorf tubes (Cat # 05,408,129, Thermo Fisher Scientific) with 1 scoop of 0.9–2.0 mm stainless steel beads, and 5 individual 3.2 mm stainless steel beads (Cat # SSB14B and SSB32, MIDSCI, Valley Park, MO, USA). In addition, 200 μl of RIPA buffer (Cat # 89,900, Thermo Fisher Scientific) with both 1:100 dilution protease inhibitor and phosphatase inhibitor (Cat # P8340 and P5726, Sigma-Aldrich Company, St. Louis, MO, USA) was added. The tissue was homogenized with a bullet blender (Cat # BBX24B, Next Advance, Troy, NY, USA) for 6 min. After homogenization, lysates were centrifuged at 12,000 RPM for 5 min and supernatants were stored at -80°C . Total protein was quantified by Bradford Assay using a SpectraMax M2e Multi-Mode microplate reader spectrophotometer (Molecular Devices, San Jose, CA, USA). Protein input was equivalent across all groups and EGFP expression was measured via ELISA (Cat # Ab171581, Abcam, Cambridge, UK). Assays were performed in duplicate per the manufacturer's instructions, and GFP ELISA was repeated to verify results ($n = 8\text{--}11$ mice per group).

Bmi1⁺ stem cell quantification by real-time PCR

Tissue was disrupted with a Fisherbrand Pellet Pestle Cordless Motor (Fisher Scientific) in Trizol (Life Technologies/Thermo Fisher). RNA was isolated using Trizol and quantitated using a Nanodrop 2000 spectrophotometer (Thermo Fisher). cDNA was synthesized from 273.5 ng of RNA using ABScript II cDNA First-Strand Synthesis Kit (ABclonal). Real-time PCR was performed using the Taq Man gene expression system (Thermo Fisher), with *Bmi1* probe (FAM) (ref seq NM_007552.4) and GAPDH probe (VIC) (ref seq NM_001289726.1, NM_008084.3) as an internal control (Appendix 1). Amplification was performed using QuantStudio 6 Real-Time PCR System (Applied Biosystems/Thermo Fisher). Real-time PCR program was as follows: hold stage of 50°C for 2 min, 95°C for 10 min, followed by a 40 cycle

PCR stage of 95°C for 15 s, 60°C for 1 min. Values for *Bmi1* and GAPDH were generated and Δct was calculated as $2^{-(\text{GAPDH}-\text{Bmi1})}$.

Experimental NEC model

Experimental NEC was based on the model described by Zani et al. [20, 21]. Heterozygous *Lgr5*^{EGFP} male mice were bred with female C57BL/6 J mice. Two groups of pups were studied: (1) breastfed controls ($n = 14$) and (2) NEC ($n = 19$). Experimental pups underwent permanent maternal separation on P5 and were taken to satellite housing in a temperature-controlled incubator. Control pups were left with their mothers to breastfeed. Pups received a total of 300 kcal/kg/day of Esbilac milk replacer (PetAg, Hampshire, IL, USA) fortified with Similac Advance powder (Similac, Columbus, OH, USA) via gavage feeding with a 1.9 French catheter. Feeds were also supplemented with 8 mg/kg lipopolysaccharide (LPS) isolated from *Escherichia Coli* O111:B4 (Cat # L4391, Sigma-Aldrich Company). Pups received stress via 5% hypoxia for 10 min three times daily, and 4°C for 12 min hypothermia twice daily. Pups were euthanized via cervical decapitation on P9. Tail cuts were saved for post-mortem genotyping.

Immunohistochemistry

Breastfed control and NEC segments of terminal ileum were harvested immediately after euthanasia and were fixed with paraformaldehyde for 36 h at 4°C and dehydrated in 70% ethanol for 24 h. After dehydration, tissues were paraffin embedded and sectioned with a microtome. Specimens were subsequently stained with a rabbit anti-GFP antibody at 1:1000 dilution (Cat # Ab6556, Abcam), as done by Todaro et al. to measure stem cell quantity [22]. The intensity of anti-GFP staining was analyzed at intestinal crypts and acted as a marker of *Lgr5*⁺-expressing ISCs. Additional segments were stained with a rabbit anti-*Bmi1*⁺ antibody at 1:200 dilution (Cat # 254,253). Staining was quantified using the IHC Profiler plugin on ImageJ [23].

Statistical analyses

Continuous data were reported as the mean and standard error of the mean (SEM). ELISA and PCR data were tested for normality and were compared using one-way ANOVA with Tukey's multiple comparisons test. Experimental NEC survival data were compared using a Log-Rank (Mantel-Cox) test, while all control and experimental NEC data were compared using the Mann-Whitney *U* test. All statistical analyses were performed, and figures were created using GraphPad Prism 8 (GraphPad Software, San Diego, CA, USA). *P* values less than 0.05 were considered significant.

Results

Duodenum

The proportion of *Lgr5*⁺ expression in the duodenum was lowest at E18 (288.1 ng GFP/g protein ± 19.4, Fig. 1A). After weaning, they continued to rise with age and peaked at P56 (2972.0 ng GFP/g protein ± 316.0, $p < 0.0001$ vs. E18). When compared to P21 (weaning age), *Lgr5*⁺-expressing ISCs were lower at days E18, 1, 3, 4, and 7 (Fig. 2A). The proportion of *Bmi1*⁺ expression also increased with age. When compared to E18, *Bmi1*⁺ expression was higher at day of life 7 ($p < 0.001$), 21 ($p < 0.05$), and 28 ($p < 0.05$, Fig. 1B).

Terminal ileum

Lgr5⁺ expression was lowest at the embryonic stages (E15 = 395.8 ng GFP/g protein ± 43.2, E18 = 392.9 ng GFP/g protein ± 29.9, Fig. 3A). As the pups continued to age, intestinal stem cell *Lgr5*⁺ peaked at P21 (5564.0 ng GFP/g protein ± 727.0, $p < 0.0001$ vs. E15). After weaning at P21 (5564 ng GFP/g protein ± 727), the proportion of *Lgr5* expression decreased and continued to drop until the oldest age point assessed (3770.0 ng GFP/g

protein ± 473.2, $p < 0.05$, Fig. 3A). The proportion of *Bmi1*⁺ expression also increased with age in the terminal ileum. When compared to E18, *Bmi1*⁺ expression was higher at all other assessed timepoints ($p < 0.05$, Fig. 3B).

Colon

In the ascending colon, *Lgr5*⁺ expression was lowest at the embryonic stages (E15 = 105.6 ng GFP/g protein ± 11.6, E18 = 237.4 ng GFP/g protein ± 22.1, Fig. 4A). After birth, *Lgr5*⁺ expression increased significantly and peaked at P7 (1767.0 ng GFP/g protein ± 193.1, $p < 0.0001$ vs. E15) and remained elevated with breastmilk exposure. After weaning at P21, the *Lgr5*⁺-expressing ISC population was still higher than in embryonic stages, but was not statistically different from P21 (Fig. 4A). The proportion of *Bmi1*⁺ expression also increased with age in the colon. When compared to E15, *Bmi1*⁺ expression was higher at the day of life 14, 21, 28, and 56 ($p < 0.05$). When compared to P21, days E15, E18, 3, and 7 were significantly lower ($p < 0.05$). *Bmi1*⁺ expression in the days following weaning was not significantly different than P21 (Fig. 4B).

Fig. 2 Intestinal stem cell markers in the duodenum. **A** *Lgr5*⁺-expressing ISCs in the duodenum increase with age and peak at P56. **B** *Bmi1*⁺ is lower in the immediate neonatal period but increases in the first weeks of life. * $p < 0.05$ vs. E18, # $p < 0.05$ vs. P21

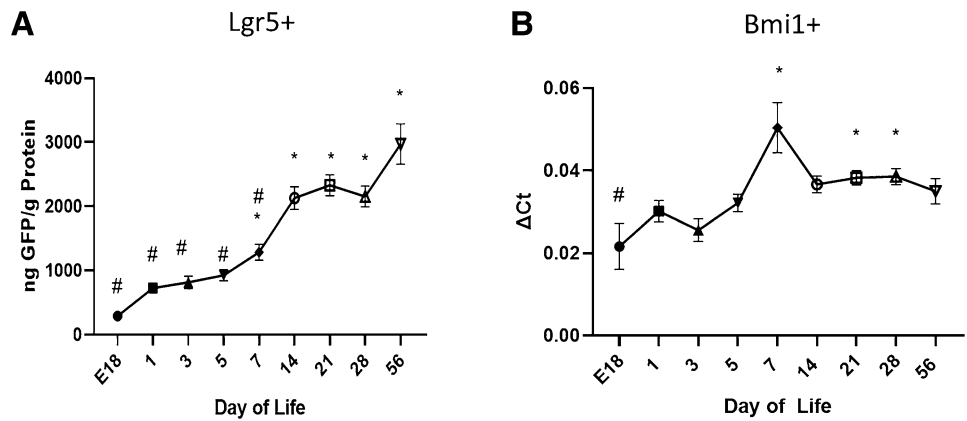


Fig. 3 Intestinal stem cell markers in the terminal ileum. **A** *Lgr5*-expressing and **B** *Bmi1*⁺-expressing ISCs in the terminal ileum increase with age * $p < 0.05$ vs. E15, # $p < 0.05$ vs. P21

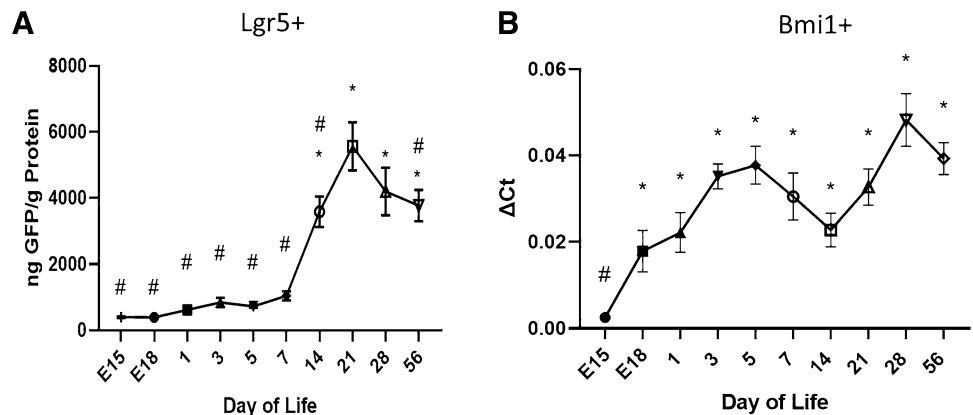
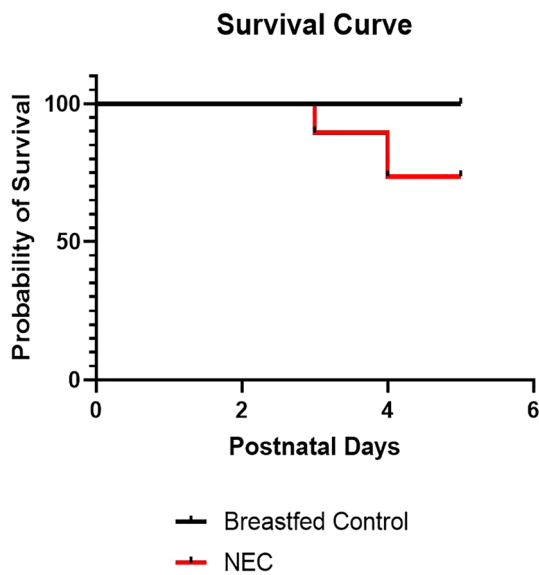
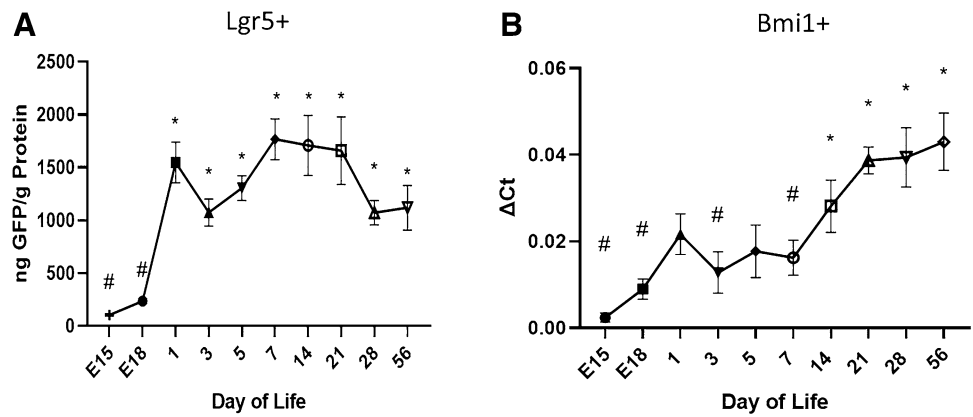


Fig. 4 Intestinal stem cell markers in the colon. **A** *Lgr5*-expressing and **B** *Bmi1*⁺-expressing ISCs in the terminal ileum increase with age **p*<0.05 vs. E15, #*p*<0.05 vs. P21



Experimental NEC

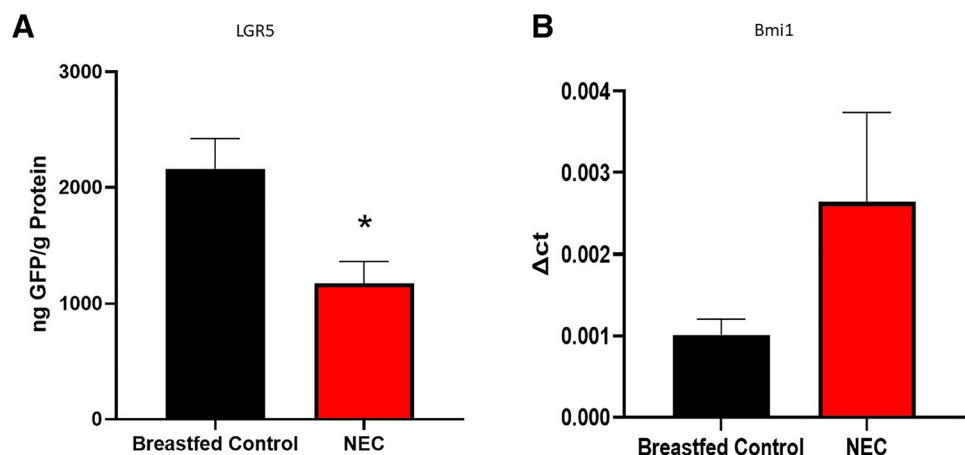
Overall mortality from experimental NEC was 26.3% (*p*=0.04 vs. breastfed control, Fig. 5). After undergoing experimental NEC, pups had a decreased expression of *Lgr5* in the terminal ileum when compared to breastfed controls (NEC = 1174 ng GFP/g protein ± 188.3, breastfed control = 2162.0 ± 259.1 ng GFP/g protein, *p*=0.0023, Fig. 6A). Analysis of *Bmi1*⁺ expression by PCR noted a higher mean value in the NEC group, but this was not statistically different from breastfed controls (*p*=0.53, Fig. 6B). When comparing the change in immunostaining between breastfed controls and those with NEC (Breastfed control minus NEC), there was a higher loss of *Lgr5*⁺ staining (Fig. 7A, B-Delta *Lgr5*) compared to *Bmi1*⁺ staining (Fig. 7C, D-Delta *Bmi1*) (*p*=0.004).

Fig. 5 NEC decreases survival. Survival curve demonstrating increased mortality for pups undergoing NEC experiment

Discussion

A plethora of endocrine, paracrine, and transcription factors orchestrate intestinal morphogenesis from the embryonic stage through adulthood. The involvement of factors regulating proliferation and differentiation during the neonatal

Fig. 6 Changes in ISC populations with NEC. **A** *Lgr5*-expressing ISCs in the terminal ileum were decreased after experimental NEC. **B** *Bmi1*⁺-expressing ISCs in the terminal ileum were not significantly altered after experimental NEC. **p*<0.05 vs. breastfed control



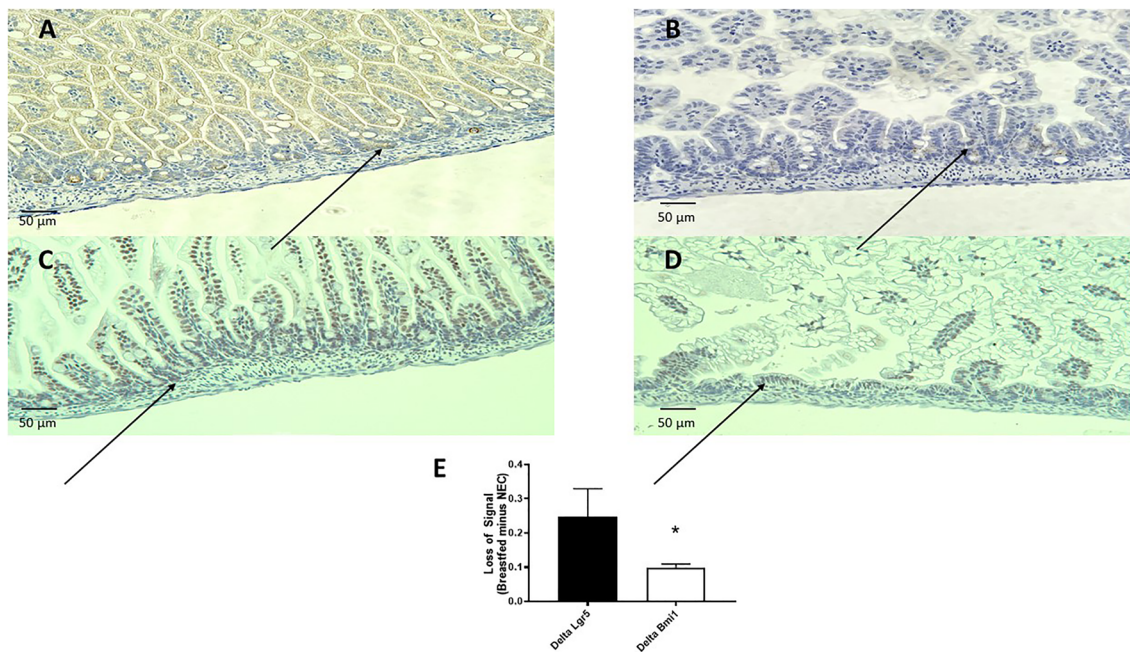


Fig. 7 *Lgr5*⁺ loss is more prominent in NEC. Representative immunohistochemistry-stained images of **A** *Lgr5*⁺ breastfed control and **B** NEC, as well as *Bmi1*⁺ **C** breastfed control and **D** NEC. The loss of *Lgr5*⁺ staining as measured by Image J between breastfed and NEC

pups (Delta *Lgr5*) was significantly more pronounced than *Bmi1*⁺ staining in the same population (Delta *Bmi1*). *= $p < 0.05$ vs. Delta *Lgr5*. Arrow represents positive staining

period declines over time during maturation to adulthood, suggesting that adult stem cells have unique requirements of factors and cofactors for intestinal stem cell maintenance and function distinct from what roles were predominant during the early neonatal period [24].

The control of intestinal stem cell proliferation, differentiation, and self-renewal in the postnatal period is regulated by multiple developmental pathways, which are likely evolutionarily conserved. These include Hedgehog, BMP, Wnt, and Notch signaling cascades. These pathways work to help form the intestinal crypts, separate the cells into different cell types, and promote the development of the intestinal villus. For example, *Sox9*, a transcription factor located downstream of Wnt, is expressed throughout the epithelium as early as embryonic day E13.5 but becomes restricted to the crypts in the adult intestines. *Sox9* represses *Cdx2* and *Muc2*, which are two genes that assist in intestinal differentiation. Other factors that likely regulate ISC development include various hormones, such as thyroid hormone, which significantly increases immediately after birth. Elevations in thyroid hormone coincide with alterations in *Blimp1*, which is strongly expressed throughout the intestine in fetal stages but becomes restricted to the intervillous regions in neonates [24].

The pathophysiology of necrotizing enterocolitis is multifactorial, complex, and remains poorly understood [25]. It is critical to better understand the disease process to discern

why preterm infants are heavily affected by this devastating disease. In our study, we observed that the *Lgr5*⁺ and *Bmi1*⁺ expression was lowest in embryonic mice in all segments of the intestine that were studied. These markers, which represent the ISC populations, appeared to increase with age until peaking sometime in the first month of life. These low cell numbers in the embryonal stage and early postnatal period may prevent infants from mounting an appropriate response to injury, thereby making them more susceptible to the effects of NEC.

The quantity of *Lgr5* expression was most interesting in the terminal ileum, where it remained in lower quantity for an extended period of time (E15–P7) and then underwent a sharp increase at P21. *Lgr5* expression became less populous immediately after weaning and continued to decline as the mice aged. These data may help to shed light on additional mechanisms of terminal ileal susceptibility, which may include fewer ISCs to repopulate the gut in this region after injury.

While there is currently no targeted medical therapy for NEC, breastmilk is known to reduce the incidence of NEC [26–28]. There are currently different theories on the mechanism of how breastmilk prevents infants from developing NEC, but it may act by altering the microbiome or increasing mesenteric perfusion [29–31]. Our data demonstrated an association between higher levels of *Lgr5* expression within the terminal ileum with exposure to breastmilk and a

decrease in this expression following weaning. Therefore, as suggested by Chen et al., an additional protective property of breastmilk may be to increase the population of ISCs [32]. Further studies are certainly needed.

Although the provision of breastmilk to preterm infants is one of the most widely studied preventative strategies for NEC, other therapies may be as equally important. Probiotics have been shown in numerous studies to protect infants from necrotizing enterocolitis [33–35]. Furthermore, modulation of the intestinal microbiome also appears to have effects on the intestinal stem cell niche [36, 37]. Therefore, it is possible that probiotics administered to preterm infants may exhibit their protective effects, in part, by altering the native microbiome and modulating intestinal stem cells. Additional therapies that have shown protective effects to intestinal stem cells (in animal models) include heparin-binding epidermal growth factor-like growth factor and mesenchymal stem cell therapy [32, 38].

Lastly, we noted an association between a significant loss of *Lgr5*⁺ expression in the terminal ileum for mice undergoing experimental NEC. The terminal ileum is traditionally at-risk during NEC, possibly due to lower blood flow in this area [39–41]. Our data contribute to these findings by suggesting that lower numbers of ISCs in the early postnatal period may make neonates more susceptible to NEC given that they already had a relatively low number of ISCs compared to their term counterparts. Therefore, it is possible that a correlation exists between the number of ISCs and the ability of preterm neonates to repopulate the gut with functional cells after injury. Our data did not demonstrate that experimental NEC resulted in a significant decrease in *Bmi1*⁺ expression, suggesting that *Lgr5*⁺-expressing ISCs may be more heavily affected during NEC. This finding is also consistent with previously published data, where *Bmi1*⁺ cells were more resistant to ischemic and radiation-induced injury and continued to be expressed in low populations in the terminal ileum following injury [14, 18, 42].

Therefore, our data suggest that intestinal stem cells, as measured by *Lgr5*⁺ and *Bmi1*⁺ expression within the intestines, are lowest in the embryonal and early postnatal periods and increase with age. The change in *Lgr5*⁺ expression between NEC and breastfed control mice was more robust than *Bmi1*⁺, suggesting that the *Lgr5*⁺ ISC population may be more involved in NEC pathogenesis than the *Bmi1*⁺ population.

Limitations

There are several limitations to this study. First, the measurement of *Lgr5* and *Bmi1*⁺ expression had higher variability in the postnatal groups compared to the embryonal groups. This may have been due to the presence of stool burden in the intestines in the postnatal groups. The Bradford assay

may have also been measuring proteins present in the stool as well as the bowel, causing more variability in the data when compared to embryonal groups. The intestines were thoroughly flushed with saline prior to being frozen to minimize this effect, and the data may have been less variable for the embryologic ages given that there was no stool in the colon.

Second, we measured markers of ISCs by measuring the expression of *Lgr5*^{EGFP} mutant surface protein, and *Bmi1* + RNA rather than directly measuring *Lgr5* and *Bmi1*. Using a protein or RNA level as a surrogate marker for cell populations may not always be accurate and could even be misleading, as cells may increase in number while simultaneously downregulating a surface protein. Conversely, cells may be injured and decrease in number and upregulate a particular surface protein to compensate. One may argue it is more accurate to measure cell count by measuring *Lgr5*⁺ or *Bmi1*⁺ expression with flow cytometry, as shown by Nigmatullina et al. [43]. Given that we measured ISC populations in 10 ages of mice in 3 different portions of bowel, flow cytometry would have been challenging and cumbersome. In addition, we did not assess whether the presence of this knock-in mutation affected native *Lgr5*⁺ ISCs in the bowel. However, the use of this same heterozygous *Lgr5*^{EGFP} transgenic mouse to measure *Lgr5*^{EGFP} as a surrogate marker of the *Lgr5*⁺-ISC population has been performed and demonstrated to be accurate [19].

Future directions

Most of our previous work has studied the effectiveness of mesenchymal stem cells (MSCs) for the treatment of intestinal ischemia and necrotizing enterocolitis [44–47]. The paracrine release of hydrogen sulfide gas is thought to be a major contributor to the effectiveness of these stem cells [45, 48–51]. MSCs and hydrogen sulfide compounds bring about increased mesenteric perfusion and improved functional outcomes in models of intestinal ischemia and NEC. It is unknown though, how hydrogen sulfide impacts the intestinal stem cell niche. It is possible that hydrogen sulfide works to protect intestinal stem cells so that they can participate in intestinal restitution during injury. Future studies will examine the impact of MSCs and hydrogen sulfide compounds on intestinal stem cells and their ability to facilitate repopulation of the gut following injury.

Conclusion

Markers of the intestinal stem cell population, such as *Lgr5* and *Bmi1*, are lowest in embryonal and early postnatal mice and appear to increase with age. In addition, a

loss of *Lgr5*⁺ expression was associated with experimental necrotizing enterocolitis, suggesting that the *Lgr5*⁺-expressing intestinal stem cell population may be involved in NEC pathogenesis. Conversely, *Bmi1*⁺ expression did not significantly decrease in number after experimental NEC, suggesting that this cell population may be relatively resistant to NEC. As the search for a targeted medical treatment for NEC continues, this study demonstrates the importance of developing a therapy to protect the already low population of ISCs in neonatal infants, so they can promote tissue recovery and regeneration after injury.

Appendix

Primers (5' → 3').

Primer	Primer sequences
GPR49-1	CGACAACCACTACCTGAGCA
GPR49-2	CGGGACCAGATGCGATA
GPR49-3	AGCTAGGCTCTGCTCTGTCA
<i>Bmi1</i>	TAGACTTTTCTCGAGGTTTTCATGGTG TTACCTAAGACAAAAGACATCTCACCC TCTATGATGGACTTACTTCTGAGAGTG CGTTTGAGGCATTATGGCTTACTAAG CAGTGTGTCAACCATACTGAAAACACT TCCATTTA TTGTATCTGGGATGAGGC TTTTTACCCTTACTCAATTTGA AAATG C TTAAGCTTAAATGATATTTTCAGTC AAAATTTGTCTTTTAATAAAACAACAG AAAGATG
GAPDH	AGCTCCCCCACCATCCGGGTTCCCTA TAAATACGGACTGCAGCCCTCCCTGGT GCTCTCTGCTCCTCCCTGTTCCAGAGA CGGCCGCATCTTCTTGTGCAGTGCCAG CCTCGTCCCGTAGACAAAATGGTGAAG GTCGGT GTGAACGGATTTGGCCGTATT GGGCGCCTGGTCACCAGGGCTGCCA TTTGACAGTGGCAAAGTGGAGATTGTTG CCATCAACGACCCCTTCAT TGACCT CAACTACATGGTCTACATGTTCCAGTA TGACTCCACTCACGG CAAATTCACCG CACAGTCA

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Declarations

Conflict of interest TAM receives consulting fees from Noveome Biotherapeutics. There is no direct conflict with the information presented in this manuscript.

Ethical approval All animal work in this study followed an IACUC-approved protocol at the Indiana University School of Medicine.

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